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tgtgtgtgat	tcctgccaga	cagcatcggc	ggggcgcgcc	gacacaacac	atagtcagat												120	
agaggagact	tcc	gtg	ccg	aac	cga	cgc	cga	cgc	aag	ctt	tcg	aca	gcc					169
		Val	Pro	Asn	Arg	Arg	Arg	Arg	Lys	Leu	Ser	Thr	Ala					
	1					5					10							
atg	agc	gcg	gtc	gcc	gcc	ctg	gca	gtg	gcg	agt	cct	tgc	gca	tac	ttc			217
Met	Ser	Ala	Val	Ala	Ala	Leu	Ala	Val	Ala	Ser	Pro	Cys	Ala	Tyr	Phe			
	15						20					25						
ctt	gtc	tac	gaa	tcg	acg	gcc	ggc	aac	aag	gcg	ccc	gag	cac	cac	gag			265
Leu	Val	Tyr	Glu	Ser	Thr	Ala	Gly	Asn	Lys	Ala	Pro	Glu	His	His	Glu			
	30					35					40							
ttc	aag	cag	gcc	gca	gtg	atg	agc	gat	ctg	ccg	ggc	gag	ctg	atg	ggc			313
Phe	Lys	Gln	Ala	Ala	Val	Met	Ser	Asp	Leu	Pro	Gly	Glu	Leu	Met	Gly			
45					50					55				60				
gcg	ctg	tcg	cag	ggc	ctg	tcg	cag	ttt	ggg	atc	aac	ctg	ccc	ccg	gtg			361
Ala	Leu	Ser	Gln	Gly	Leu	Ser	Gln	Phe	Gly	Ile	Asn	Leu	Pro	Pro	Val			
				65				70					75					

ccc gcc ctg agc ggc ggc gcc acc agc act ccc ggt ctg gcc agc ccc Pro Ala Leu Ser Gly Gly Ala Thr Ser Thr Pro Gly Leu Ala Ser Pro 80 85 90	409
ggc ctg ggt agc ccc ggc ctg ggc acg ccc ggc ctg gga acg ccg ggc Gly Leu Gly Ser Pro Gly Leu Gly Thr Pro Gly Leu Gly Thr Pro Gly 95 100 105	457
ctg acc aat ccc ggt ctg acg agc ccc ggt gcg acc agt ccc ggc ctg Leu Thr Asn Pro Gly Leu Thr Ser Pro Gly Ala Thr Ser Pro Gly Leu 110 115 120	505
acc agt ccc ggc ctg acc agt cct ggt ttg acc agc ccc ggt ctg acc Thr Ser Pro Gly Leu Thr Ser Pro Gly Leu Thr Ser Pro Gly Leu Thr 125 130 135 140	553
agc ccg ggt gcg gcg ccg acg acg ccc ggg ctc acc gcg ccc ggc gcg Ser Pro Gly Ala Ala Pro Thr Thr Pro Gly Leu Thr Ala Pro Gly Ala 145 150 155	601
ctg ccg acc acg ccg ggc ggc ggg gtc gcc acc ccc ggc gcc ggg ctc Leu Pro Thr Thr Pro Gly Gly Gly Val Ala Thr Pro Gly Ala Gly Leu 160 165 170	649
aac ccc gcg ctg tcc aac ccc ggg ctg acc agc ccg gcc ggg acg gcg Asn Pro Ala Leu Ser Asn Pro Gly Leu Thr Ser Pro Ala Gly Thr Ala 175 180 185	697
ccg ggg ctg ggc agc ccg acc gtg gcg ccg agt gag gtg ccg atc gac Pro Gly Leu Gly Ser Pro Thr Val Ala Pro Ser Glu Val Pro Ile Asp 190 195 200	745
tcc ggg gcc ggc ctg gac ccg ggc gcc ggt ggc acg tac ccg atc ctg Ser Gly Ala Gly Leu Asp Pro Gly Ala Gly Gly Thr Tyr Pro Ile Leu 205 210 215 220	793
ggc gac ccg tcg acc ttc ggt aac gcc tcg ccg atc ggc ggc ggt ggc Gly Asp Pro Ser Thr Phe Gly Asn Ala Ser Pro Ile Gly Gly Gly Gly 225 230 235	841
acc ggt ctg ggc ggc ggc tcg agc tcg ggt ggc agc ggc ggc ctg gtc Thr Gly Leu Gly Gly Ser Ser Ser Gly Gly Ser Gly Gly Leu Val 240 245 250	889
aac gac gtg atg caa gcc gcc aac cag ctc ggc gcg ggt cag gcg atc Asn Asp Val Met Gln Ala Ala Asn Gln Leu Gly Ala Gly Gln Ala Ile 255 260 265	937
gac ctg ctc aag ggc ctg gtg atg ccg gcg atc acg cag ggc atg cac Asp Leu Leu Lys Gly Leu Val Met Pro Ala Ile Thr Gln Gly Met His 270 275 280	985
ggc ggc gcg gcc gcg ggt gct ttg ccc ggc gcg gcc ggt gct ctg ccc Gly Gly Ala Ala Ala Gly Ala Leu Pro Gly Ala Ala Gly Ala Leu Pro 285 290 295 300	1033
ggc gcg gcc ggc gcc ctg ccc ggt gcg gcc ggc gcc ctg ccg ggt gcg Gly Ala Ala Gly Ala Leu Pro Gly Ala Ala Gly Ala Leu Pro Gly Ala 305 310 315	1081
gcg ggc gcc gcg ggt gcg ttg ccg gcg gcc gcc ggc gcc gcg ccg gca Ala Gly Ala Ala Gly Ala Leu Pro Ala Ala Ala Gly Ala Ala Pro Ala 320 325 330	1129
ctg ccc ccg gtc tag accttttcca aaccatccac cagacggcac c Leu Pro Val 335	1175

<210> 2

<211> 336

<212> PRT

<213> mycobacterium avium paratuberculosis

<400> 2

Val Pro Asn Arg Arg Arg Arg Lys Leu Ser Thr Ala Met Ser Ala Val
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Ala Ala Leu Ala Val Ala Ser Pro Cys Ala Tyr Phe Leu Val Tyr Glu
 20 25 30

Ser Thr Ala Gly Asn Lys Ala Pro Glu His His Glu Phe Lys Gln Ala
 35 40 45

Ala Val Met Ser Asp Leu Pro Gly Glu Leu Met Gly Ala Leu Ser Gln
 50 55 60

Gly Leu Ser Gln Phe Gly Ile Asn Leu Pro Pro Val Pro Ala Leu Ser
 65 70 75 80

Gly Gly Ala Thr Ser Thr Pro Gly Leu Ala Ser Pro Gly Leu Gly Ser
 85 90 95

Pro Gly Leu Gly Thr Pro Gly Leu Gly Thr Pro Gly Leu Thr Asn Pro
 100 105 110

Gly Leu Thr Ser Pro Gly Ala Thr Ser Pro Gly Leu Thr Ser Pro Gly
 115 120 125

Leu Thr Ser Pro Gly Leu Thr Ser Pro Gly Leu Thr Ser Pro Gly Ala
 130 135 140

Ala Pro Thr Thr Pro Gly Leu Thr Ala Pro Gly Ala Leu Pro Thr Thr
 145 150 155 160

Pro Gly Gly Gly Val Ala Thr Pro Gly Ala Gly Leu Asn Pro Ala Leu
 165 170 175

Ser Asn Pro Gly Leu Thr Ser Pro Ala Gly Thr Ala Pro Gly Leu Gly
 180 185 190

Ser Pro Thr Val Ala Pro Ser Glu Val Pro Ile Asp Ser Gly Ala Gly
 195 200 205

Leu Asp Pro Gly Ala Gly Gly Thr Tyr Pro Ile Leu Gly Asp Pro Ser
 210 215 220

Thr Phe Gly Asn Ala Ser Pro Ile Gly Gly Gly Gly Thr Gly Leu Gly
225 230 235 240

Gly Gly Ser Ser Ser Gly Gly Ser Gly Gly Leu Val Asn Asp Val Met
245 250 255

Gln Ala Ala Asn Gln Leu Gly Ala Gly Gln Ala Ile Asp Leu Leu Lys
260 265 270

Gly Leu Val Met Pro Ala Ile Thr Gln Gly Met His Gly Gly Ala Ala
275 280 285

Ala Gly Ala Leu Pro Gly Ala Ala Gly Ala Leu Pro Gly Ala Ala Gly
290 295 300

Ala Leu Pro Gly Ala Ala Gly Ala Leu Pro Gly Ala Ala Gly Ala Ala
305 310 315 320

Gly Ala Leu Pro Ala Ala Ala Gly Ala Ala Pro Ala Leu Pro Pro Val
325 330 335

<210> 3

<211> 600

<212> DNA

<213> mycobacterium avium paratuberculosis

<220>

<221> CDS

<222> (67)..(567)

<223>

<400> 3

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cagggc atg tcc cgt ttg tca ttt gtc tgc agg ctt ttg gcc gca acc 108
Met Ser Arg Leu Ser Phe Val Cys Arg Leu Leu Ala Ala Thr
1 5 10

gct ttc gcc gtc gcc ctg cta ctc ggg ctg ggc gac gtg ccg cgc gcg 156
Ala Phe Ala Val Ala Leu Leu Leu Gly Leu Gly Asp Val Pro Arg Ala
15 20 25 30

gcg gcc acc gac gac cgc ctg caa ttc acc gcg acc acg ctc agc ggc 204
Ala Ala Thr Asp Asp Arg Leu Gln Phe Thr Ala Thr Thr Leu Ser Gly
35 40 45

gcg ccg ttc aac ggc gcc agt ctg cag ggc aag ccc gcc gtg ctg tgg 252
Ala Pro Phe Asn Gly Ala Ser Leu Gln Gly Lys Pro Ala Val Leu Trp
50 55 60

ttc tgg acg ccg tgg tgc ccg tac tgc aac gcc gag gcc ccg ggc gtg 300
 Phe Trp Thr Pro Trp Cys Pro Tyr Cys Asn Ala Glu Ala Pro Gly Val
 65 70 75
 agc cgg gtg gcc gcc gcc aac ccg ggc gtc acc ttc gtc ggc gtc gcc 348
 Ser Arg Val Ala Ala Ala Asn Pro Gly Val Thr Phe Val Gly Val Ala
 80 85 90
 gcc cac tcc gaa gtc ggc gcc atg gcc aac ttc gtc tcc aag tac aac 396
 Ala His Ser Glu Val Gly Ala Met Ala Asn Phe Val Ser Lys Tyr Asn
 95 100 105 110
 ctg aac ttc acc acg ctc aac gac gcc gac ggc gcg atc tgg gcc cgc 444
 Leu Asn Phe Thr Thr Leu Asn Asp Ala Asp Gly Ala Ile Trp Ala Arg
 115 120 125
 tac ggc gtg ccc tgg cag ccc gcg tac gtg ttc tac ccg gcg gac gcc 492
 Tyr Gly Val Pro Trp Gln Pro Ala Tyr Val Phe Tyr Arg Ala Asp Gly
 130 135 140
 agc tcc acc ttc gtc aac aac ccc acc tcg gcg atg ccc cag gac gaa 540
 Ser Ser Thr Phe Val Asn Asn Pro Thr Ser Ala Met Pro Gln Asp Glu
 145 150 155
 ctg gcc gcc ccg gtg gcg gcg ctg cgc tgacgtggac cgcggtctgg 587
 Leu Ala Ala Arg Val Ala Ala Leu Arg
 160 165
 tcgggctggc ggt 600

<210> 4

<211> 167

<212> PRT

<213> mycobacterium avium paratuberculosis

<400> 4

Met Ser Arg Leu Ser Phe Val Cys Arg Leu Leu Ala Ala Thr Ala Phe
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 Ala Val Ala Leu Leu Leu Gly Leu Gly Asp Val Pro Arg Ala Ala Ala
 20 25 30
 Thr Asp Asp Arg Leu Gln Phe Thr Ala Thr Thr Leu Ser Gly Ala Pro
 35 40 45
 Phe Asn Gly Ala Ser Leu Gln Gly Lys Pro Ala Val Leu Trp Phe Trp
 50 55 60
 Thr Pro Trp Cys Pro Tyr Cys Asn Ala Glu Ala Pro Gly Val Ser Arg
 65 70 75 80
 Val Ala Ala Ala Asn Pro Gly Val Thr Phe Val Gly Val Ala Ala His
 85 90 95

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Ser Glu Val Gly Ala Met Ala Asn Phe Val Ser Lys Tyr Asn Leu Asn
 100 105 110

Phe Thr Thr Leu Asn Asp Ala Asp Gly Ala Ile Trp Ala Arg Tyr Gly
 115 120 125

Val Pro Trp Gln Pro Ala Tyr Val Phe Tyr Arg Ala Asp Gly Ser Ser
 130 135 140

Thr Phe Val Asn Asn Pro Thr Ser Ala Met Pro Gln Asp Glu Leu Ala
 145 150 155 160

Ala Arg Val Ala Ala Leu Arg
 165

<210> 5

<211> 366

<212> DNA

<213> mycobacterium avium paratuberculosis

<220>

<221> CDS

<222> (34) .. (366)

<223>

<400> 5

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Met Arg Leu Ser Leu Ser Lys	
1 5	
ttg ggc gtt gcg gtg ggc agc gcg gca gtg gca ttg acc gcc gcg gcc	102
Leu Gly Val Ala Val Gly Ser Ala Ala Val Ala Leu Thr Ala Ala Ala	
10 15 20	
ggg gtc gca tcc gcc gac ccc atg gac gcg atc atc aac acc acc tgc	150
Gly Val Ala Ser Ala Asp Pro Met Asp Ala Ile Ile Asn Thr Thr Cys	
25 30 35	
aac tac ggg cag gtg atc gcc gcg ctg aac gcg tcc gac ccg gcg gct	198
Asn Tyr Gly Gln Val Ile Ala Ala Leu Asn Ala Ser Asp Pro Ala Ala	
40 45 50 55	
gcc cag cag ctg aac tcg tcg ccg atg gcg cag tcc tac atc cag cgg	246
Ala Gln Gln Leu Asn Ser Ser Pro Met Ala Gln Ser Tyr Ile Gln Arg	
60 65 70	
ttc ctg gcc tcc ccg ccg gcg aag cgt cag cag atg gcc cag cag atc	294
Phe Leu Ala Ser Pro Pro Ala Lys Arg Gln Gln Met Ala Gln Gln Ile	
75 80 85	
cag ggc atg ccg gcc gcg cag cag tac atc aac gac atc aac cag gtc	342
Gln Gly Met Pro Ala Ala Gln Gln Tyr Ile Asn Asp Ile Asn Gln Val	
90 95 100	

gcg gtc acc tgt aac aac ttc tga
Ala Val Thr Cys Asn Asn Phe
105 110

366

<210> 6

<211> 110

<212> PRT

<213> mycobacterium avium paratuberculosis

<400> 6

Met Arg Leu Ser Leu Ser Lys Leu Gly Val Ala Val Gly Ser Ala Ala
1 5 10 15

Val Ala Leu Thr Ala Ala Ala Gly Val Ala Ser Ala Asp Pro Met Asp
20 25 30

Ala Ile Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Ile Ala Ala Leu
35 40 45

Asn Ala Ser Asp Pro Ala Ala Ala Gln Gln Leu Asn Ser Ser Pro Met
50 55 60

Ala Gln Ser Tyr Ile Gln Arg Phe Leu Ala Ser Pro Pro Ala Lys Arg
65 70 75 80

Gln Gln Met Ala Gln Gln Ile Gln Gly Met Pro Ala Ala Gln Gln Tyr
85 90 95

Ile Asn Asp Ile Asn Gln Val Ala Val Thr Cys Asn Asn Phe
100 105 110

<210> 7

<211> 1410

<212> DNA

<213> mycobacterium avium paratuberculosis

<220>

<221> CDS

<222> (46)..(1410)

<223>

<400> 7

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57

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Val Ser Ser Asp Leu Phe Ser Gln Ile Val Asn Ser Gly Pro Gly Ser																
5 10 15 20																
ttt ctc gcc aag cag ctc ggc gtc ccg caa ccc gag acg ctg cgc cgc	153															
Phe Leu Ala Lys Gln Leu Gly Val Pro Gln Pro Glu Thr Leu Arg Arg																
25 30 35																
tac cgg ccc ggt gac ccg ccg ctg gcc ggg tcc ctg ctg atc ggc ggc	201															
Tyr Arg Pro Gly Asp Pro Pro Leu Ala Gly Ser Leu Leu Ile Gly Gly																
40 45 50																
gag ggc cgc gtg gtc gag ccg ctg ccg gcg gcg ctg gcc aag gac tac	249															
Glu Gly Arg Val Val Glu Pro Leu Arg Ala Ala Leu Ala Lys Asp Tyr																
55 60 65																
gac ctg gtc ggc aac aac ctg ggc ggg cgc tgg gcc gac ccg ttc ggc	297															
Asp Leu Val Gly Asn Asn Leu Gly Gly Arg Trp Ala Asp Arg Phe Gly																
70 75 80																
ggg ctg gtc ttc gac gcc acc ggg atc acc acc ccg gag ggc ctg aag	345															
Gly Leu Val Phe Asp Ala Thr Gly Ile Thr Thr Pro Glu Gly Leu Lys																
85 90 95 100																
ggg ctg tac gag ttc ttc acc cca ctg ctg cgc aac ctg ggt cac tgc	393															
Gly Leu Tyr Glu Phe Phe Thr Pro Leu Leu Arg Asn Leu Gly His Cys																
105 110 115																
gcc cgc gtg gtg gtc ggc acc acg ccc gac gcc gcc gcc ggc ccg	441															
Ala Arg Val Val Val Val Gly Thr Thr Pro Asp Ala Ala Ala Gly Pro																
120 125 130																
cac gag ccg atc gcc cag cgc gcc ctg gag ggc ttc acc ccg tca ttg	489															
His Glu Arg Ile Ala Gln Arg Ala Leu Glu Gly Phe Thr Arg Ser Leu																
135 140 145																
ggc aag gag ctg cgc aac ggc tcc acg gtg gcg ctg gtg tac ctg tcc	537															
Gly Lys Glu Leu Arg Asn Gly Ser Thr Val Ala Leu Val Tyr Leu Ser																
150 155 160																
ccg gcc gcc aaa ccc gcc gcg acg ggc ctg gag tcc acc atg ccg ttc	585															
Pro Ala Ala Lys Pro Ala Ala Thr Gly Leu Glu Ser Thr Met Arg Phe																
165 170 175 180																
atc ctg tcc gcc aag tcc gcc tac gtc gac ggc cag gtc ttc tac gtc	633															
Ile Leu Ser Ala Lys Ser Ala Tyr Val Asp Gly Gln Val Phe Tyr Val																
185 190 195																
ggc gag gcc gac tcc acc ccc ccg gcg gac tgg gaa ccg ccg ctg gac	681															
Gly Glu Ala Asp Ser Thr Pro Pro Ala Asp Trp Glu Arg Pro Leu Asp																
200 205 210																
ggc aag gtc gcc atc gtg acc ggt gcg gcc cgc gga atc ggc gcc acg	729															
Gly Lys Val Ala Ile Val Thr Gly Ala Ala Arg Gly Ile Gly Ala Thr																
215 220 225																
atc gcc gag gtg ttc gcc cgc gac ggc gcc cgc gtg gtc gcg atc gac	777															
Ile Ala Glu Val Phe Ala Arg Asp Gly Ala Arg Val Val Ala Ile Asp																
230 235 240																
gtg gaa tcc gcc gcc gag acg ctg gcc gag acg gcc agc ccg gtc ggc	825															
Val Glu Ser Ala Ala Glu Thr Leu Ala Glu Thr Ala Ser Arg Val Gly																
245 250 255 260																
ggc acc gcg ctg tgg ctc gac gtc acc gcc ccc gac gcc gtc gac aag	873															

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Gly Thr Ala Leu Trp Leu Asp Val Thr Ala Pro Asp Ala Val Asp Lys	
265 270 275	
atc acc gag cac ctg cgc gag cac cac ggc ggt cac gcc gac atc ctg	921
Ile Thr Glu His Leu Arg Glu His His Gly Gly His Ala Asp Ile Leu	
280 285 290	
gtc aac aac gcc ggg atc acc cgc gac aag ctg ctg gcc aac atg gac	969
Val Asn Asn Ala Gly Ile Thr Arg Asp Lys Leu Leu Ala Asn Met Asp	
295 300 305	
gac gcg cgc tgg gac gcc gtg ttg gcc gtg aat ctg ctt gcc cca ctt	1017
Asp Ala Arg Trp Asp Ala Val Leu Ala Val Asn Leu Leu Ala Pro Leu	
310 315 320	
cgc ctt acc gaa ggg ctg gtg ggc aac ggc agc atc ggc gaa ggc ggc	1065
Arg Leu Thr Glu Gly Leu Val Gly Asn Gly Ser Ile Gly Glu Gly Gly	
325 330 335 340	
cgc atc gtc ggc ctt tcg tcg atg gcc ggc atc gcg ggc aac cgc ggc	1113
Arg Ile Val Gly Leu Ser Ser Met Ala Gly Ile Ala Gly Asn Arg Gly	
345 350 355	
cag acc aac tac gcc acc acc aag gca ggc atg atc ggc ctc acc cag	1161
Gln Thr Asn Tyr Ala Thr Thr Lys Ala Gly Met Ile Gly Leu Thr Gln	
360 365 370	
gcg ctg gcg ccg gag ctc tac gac aag ggc atc acc atc aac gcc gtc	1209
Ala Leu Ala Pro Glu Leu Tyr Asp Lys Gly Ile Thr Ile Asn Ala Val	
375 380 385	
gcg ccg gga ttc atc gag acc cag atg acg gcc gcc atc ccg ctg gcc	1257
Ala Pro Gly Phe Ile Glu Thr Gln Met Thr Ala Ala Ile Pro Leu Ala	
390 395 400	
acc cgc gag gtg ggg cgc cgg atg aac tcg ctg ctg cag ggc ggg cag	1305
Thr Arg Glu Val Gly Arg Arg Met Asn Ser Leu Leu Gln Gly Gly Gln	
405 410 415 420	
ccg gtg gac gtc gcc gaa acc atc gcc tac ttc gcc agc ccg gcg tcg	1353
Pro Val Asp Val Ala Glu Thr Ile Ala Tyr Phe Ala Ser Pro Ala Ser	
425 430 435	
aac gcg gtg acc ggc aac gtc atc cgg gtc tgc ggc cag gcg atg ctg	1401
Asn Ala Val Thr Gly Asn Val Ile Arg Val Cys Gly Gln Ala Met Leu	
440 445 450	
ggg gca tga	1410
Gly Ala	

<210> 8

<211> 454

<212> PRT

<213> mycobacterium avium paratuberculosis

<400> 8

Val Ala Pro Lys Val Ser Ser Asp Leu Phe Ser Gln Ile Val Asn Ser
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Gly Pro Gly Ser Phe Leu Ala Lys Gln Leu Gly Val Pro Gln Pro Glu
 20 25 30

Thr Leu Arg Arg Tyr Arg Pro Gly Asp Pro Pro Leu Ala Gly Ser Leu
 35 40 45

Leu Ile Gly Gly Glu Gly Arg Val Val Glu Pro Leu Arg Ala Ala Leu
 50 55 60

Ala Lys Asp Tyr Asp Leu Val Gly Asn Asn Leu Gly Gly Arg Trp Ala
 65 70 75 80

Asp Arg Phe Gly Gly Leu Val Phe Asp Ala Thr Gly Ile Thr Thr Pro
 85 90 95

Glu Gly Leu Lys Gly Leu Tyr Glu Phe Phe Thr Pro Leu Leu Arg Asn
 100 105 110

Leu Gly His Cys Ala Arg Val Val Val Val Gly Thr Thr Pro Asp Ala
 115 120 125

Ala Ala Gly Pro His Glu Arg Ile Ala Gln Arg Ala Leu Glu Gly Phe
 130 135 140

Thr Arg Ser Leu Gly Lys Glu Leu Arg Asn Gly Ser Thr Val Ala Leu
 145 150 155 160

Val Tyr Leu Ser Pro Ala Ala Lys Pro Ala Ala Thr Gly Leu Glu Ser
 165 170 175

Thr Met Arg Phe Ile Leu Ser Ala Lys Ser Ala Tyr Val Asp Gly Gln
 180 185 190

Val Phe Tyr Val Gly Glu Ala Asp Ser Thr Pro Pro Ala Asp Trp Glu
 195 200 205

Arg Pro Leu Asp Gly Lys Val Ala Ile Val Thr Gly Ala Ala Arg Gly
 210 215 220

Ile Gly Ala Thr Ile Ala Glu Val Phe Ala Arg Asp Gly Ala Arg Val
 225 230 235 240

Val Ala Ile Asp Val Glu Ser Ala Ala Glu Thr Leu Ala Glu Thr Ala
 245 250 255

Ser Arg Val Gly Gly Thr Ala Leu Trp Leu Asp Val Thr Ala Pro Asp
 260 265 270

Ala Val Asp Lys Ile Thr Glu His Leu Arg Glu His His Gly Gly His
 275 280 285

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Ala Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg Asp Lys Leu Leu
290 295 300

Ala Asn Met Asp Asp Ala Arg Trp Asp Ala Val Leu Ala Val Asn Leu
305 310 315 320

Leu Ala Pro Leu Arg Leu Thr Glu Gly Leu Val Gly Asn Gly Ser Ile
325 330 335

Gly Glu Gly Gly Arg Ile Val Gly Leu Ser Ser Met Ala Gly Ile Ala
340 345 350

Gly Asn Arg Gly Gln Thr Asn Tyr Ala Thr Thr Lys Ala Gly Met Ile
355 360 365

Gly Leu Thr Gln Ala Leu Ala Pro Glu Leu Tyr Asp Lys Gly Ile Thr
370 375 380

Ile Asn Ala Val Ala Pro Gly Phe Ile Glu Thr Gln Met Thr Ala Ala
385 390 395 400

Ile Pro Leu Ala Thr Arg Glu Val Gly Arg Arg Met Asn Ser Leu Leu
405 410 415

Gln Gly Gly Gln Pro Val Asp Val Ala Glu Thr Ile Ala Tyr Phe Ala
420 425 430

Ser Pro Ala Ser Asn Ala Val Thr Gly Asn Val Ile Arg Val Cys Gly
435 440 445

Gln Ala Met Leu Gly Ala
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<210> 9

<211> 625

<212> DNA

<213> mycobacterium avium paratuberculosis

<220>

<221> misc_feature

<222> (592)..(592)

<223> "n"

<220>

<221> CDS

<222> (179)..(625)

<223>

<220>

<221> misc_feature

<222> (619)..(619)

<223> "n"

<400> 9

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gtcaatccgg atcggacccc aacgtcgact tgtgggcgcc aattcgcggg ttttcgccca      120
gcaagtcgac gttcggcgcg aatcgggtgag gtgggcacag gtgaatgacg aagaggac      178

atg ctg gtc gcc acg gtg cgg gcg ttc atc gac cgc gag gtc aaa ccg      226
Met Leu Val Ala Thr Val Arg Ala Phe Ile Asp Arg Glu Val Lys Pro
1          5          10          15

acc gtg cgc gag gtg gag cac gcc gat gcc tat ccc gag gcg tgg atc      274
Thr Val Arg Glu Val Glu His Ala Asp Ala Tyr Pro Glu Ala Trp Ile
20          25          30

gag cag atg aag cgg atc ggg atc tac ggg ctg gcg gtg ccc gag gaa      322
Glu Gln Met Lys Arg Ile Gly Ile Tyr Gly Leu Ala Val Pro Glu Glu
35          40          45

tac ggt ggt tcg ccg gtg tcc atg ccg tgc tac gtg cgg gtc acc gag      370
Tyr Gly Gly Ser Pro Val Ser Met Pro Cys Tyr Val Arg Val Thr Glu
50          55          60

cag ctg gcg cgc ggc tgg atg agc ctg gcc ggg gcg atg ggc ggg cac      418
Gln Leu Ala Arg Gly Trp Met Ser Leu Ala Gly Ala Met Gly Gly His
65          70          75          80

acc gtg gtg gcc aag ctg cta acg ctg ttc ggc acc gag gac cas aag      466
Thr Val Val Ala Lys Leu Leu Thr Leu Phe Gly Thr Glu Asp Xaa Lys
85          90          95

cgg gcc tac ctg ccg cgg atg gcc agc ggc gaa atc cgg gcc acc atg      514
Arg Ala Tyr Leu Pro Arg Met Ala Ser Gly Glu Ile Arg Ala Thr Met
100          105          110

gcg ttg acc gag ccc sgc ggc ggc tcg gac ctg cag aac atg tcg acc      562
Ala Leu Thr Glu Pro Xaa Gly Gly Ser Asp Leu Gln Asn Met Ser Thr
115          120          125

acc gcg ctg ccc gac ccc gac tcc gac ggn ctg gtg gtc aac ggg gcc      610
Thr Ala Leu Pro Asp Pro Asp Ser Asp Gly Leu Val Val Asn Gly Ala
130          135          140

aag acc tgn atc aac      625
Lys Thr Xaa Ile Asn
145

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<210> 10

<211> 149

<212> PRT

<213> mycobacterium avium paratuberculosis

<220>

<221> misc_feature

<222> (95)..(95)

<223> The 'Xaa' at location 95 stands for Gln, or His.

<220>

<221> misc_feature

<222> (118)..(118)

<223> The 'Xaa' at location 118 stands for Gly, or Arg.

<220>

<221> misc_feature

<222> (147)..(147)

<223> The 'Xaa' at location 147 stands for a stop codon, Trp, or Cys.

<220>

<221> misc_feature

<222> (592)..(592)

<223> "n"

<220>

<221> misc_feature

<222> (619)..(619)

<223> "n"

<400> 10

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Thr Val Arg Glu Val Glu His Ala Asp Ala Tyr Pro Glu Ala Trp Ile
20 25 30

Glu Gln Met Lys Arg Ile Gly Ile Tyr Gly Leu Ala Val Pro Glu Glu
35 40 45

Tyr Gly Gly Ser Pro Val Ser Met Pro Cys Tyr Val Arg Val Thr Glu
50 55 60

Gln Leu Ala Arg Gly Trp Met Ser Leu Ala Gly Ala Met Gly Gly His
65 70 75 80

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Thr Val Val Ala Lys Leu Leu Thr Leu Phe Gly Thr Glu Asp Xaa Lys
85 90 95

Arg Ala Tyr Leu Pro Arg Met Ala Ser Gly Glu Ile Arg Ala Thr Met
100 105 110

Ala Leu Thr Glu Pro Xaa Gly Gly Ser Asp Leu Gln Asn Met Ser Thr
115 120 125

Thr Ala Leu Pro Asp Pro Asp Ser Asp Gly Leu Val Val Asn Gly Ala
130 135 140

Lys Thr Xaa Ile Asn
145

<210> 11

<211> 241

<212> DNA

<213> mycobacterium avium paratuberculosis

<220>

<221> CDS

<222> (147)..(239)

<223>

<400> 11
gtgggggcaa gccaatcacg ttgcatcga cccggcacag gcggtcgctc acgtcatcaa 60
catgccgctc atccccgatg aggtcgaat gaccttgcta cgcaggcgct gaacgcacga 120
cgaaacggac cggaggtgaa agggac atg agc cac gcc gat caa ctc gct cgg 173
Met Ser His Ala Asp Gln Leu Ala Arg
1 5
acg cac ctg gcg ccc gat cct gcg gac ctg tcg cgc ctg gtc gcc ggc 221
Thr His Leu Ala Pro Asp Pro Ala Asp Leu Ser Arg Leu Val Ala Gly
10 15 20 25
acc cac cac gac ccg cac gg 241
Thr His His Asp Pro His
30

<210> 12

<211> 31

<212> PRT

<213> mycobacterium avium paratuberculosis

<400> 12

Met Ser His Ala Asp Gln Leu Ala Arg Thr His Leu Ala Pro Asp Pro
 1 5 10 15

Ala Asp Leu Ser Arg Leu Val Ala Gly Thr His His Asp Pro His
 20 25 30

<210> 13

<211> 236

<212> DNA

<213> mycobacterium avium paratuberculosis

<220>

<221> CDS

<222> (8)..(214)

<223>

<400> 13

ggacacc aac gtg acc ggg gtg ttt ctc acc gcc cag gcg gcg gcc cgg 49
 Asn Val Thr Gly Val Phe Leu Thr Ala Gln Ala Ala Ala Arg
 1 5 10

gcg atg atg cgg cag ggc cgc ggc gcc atc atc acc acc gcc tcg 97
 Ala Met Met Arg Gln Gly Arg Gly Gly Ala Ile Ile Thr Thr Ala Ser
 15 20 25 30

atg tcc ggg cac atc atc aac gtc ccg cag cag gtc ggc cac tac tgc 145
 Met Ser Gly His Ile Ile Asn Val Pro Gln Gln Val Gly His Tyr Cys
 35 40 45

gcc agc aag gcg gcc gtg atc cag ctg acc aag gcc atg gcc gtc gaa 193
 Ala Ser Lys Ala Ala Val Ile Gln Leu Thr Lys Ala Met Ala Val Glu
 50 55 60

ttc tgc agg atc cgt cga ctc tagactcgag caagcttatg ca 236
 Phe Cys Arg Ile Arg Arg Leu
 65

<210> 14

<211> 69

<212> PRT

<213> mycobacterium avium paratuberculosis

<400> 14

Asn Val Thr Gly Val Phe Leu Thr Ala Gln Ala Ala Ala Arg Ala Met
 1 5 10 15


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ggc ctg gcc aag ggc ggg atc acc atg ttc gac gac gac gac gcg atc      195
Gly Leu Ala Lys Gly Gly Ile Thr Met Phe Asp Asp Asp Asp Ala Ile
      45                      50                      55

ggc atg ggc cac agc gtg tgc tcg agc atc gac gcc aac ccc aac gtg      243
Ala Met Gly His Ser Val Cys Ser Ser Ile Asp Ala Asn Pro Asn Val
      60                      65                      70

tcg atg ctg gcg ctg cgg ctg acc aag caa acc ccg ttg acg ccg aag      291
Ser Met Leu Ala Leu Arg Leu Thr Lys Gln Thr Pro Leu Thr Pro Lys
      75                      80                      85

caa tcc ggc tac ttc atc ggt ctt tcg gtc gcc agc tac ntg ccc gca      339
Gln Ser Gly Tyr Phe Ile Gly Leu Ser Val Ala Ser Tyr Xaa Pro Ala
      90                      95                      100                      105

gta caa gga cga cgt cga ccc ctc gct ggg ctg gct gat ccc gcc gcc      387
Val Gln Gly Arg Arg Arg Pro Leu Ala Gly Leu Ala Asp Pro Ala Ala
      110                      115                      120

gct gat gtg ang ttg ccg gcc ggc atc ggc gt      419
Ala Asp Val Xaa Leu Pro Ala Gly Ile Gly
      125                      130

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<210> 16

<211> 131

<212> PRT

<213> mycobacterium avium paratuberculosis

<220>

<221> misc_feature

<222> (103)..(103)

<223> The 'Xaa' at location 103 stands for Met, Val, or Leu.

<220>

<221> misc_feature

<222> (125)..(125)

<223> The 'Xaa' at location 125 stands for Lys, Arg, Thr, or Met.

<220>

<221> misc_feature

<222> (331)..(331)

<223> "n"

<220>

<221> misc_feature

<222> (398)..(398)

<223> "n"

<400> 16

Met Thr His Thr Lys Ala Gly Arg Ala Ala Trp Pro Ala Ala Cys Ala
 1 5 10 15

Val Val Leu Ser Ala Ala Ala Leu Leu Cys Ala Ala Ala Ala Ala Ala
 20 25 30

Asp Glu Ala Asp Asp Ala Phe Leu Ala Gly Leu Ala Lys Gly Gly Ile
 35 40 45

Thr Met Phe Asp Asp Asp Ala Ile Ala Met Gly His Ser Val Cys
 50 55 60

Ser Ser Ile Asp Ala Asn Pro Asn Val Ser Met Leu Ala Leu Arg Leu
 65 70 75 80

Thr Lys Gln Thr Pro Leu Thr Pro Lys Gln Ser Gly Tyr Phe Ile Gly
 85 90 95

Leu Ser Val Ala Ser Tyr Xaa Pro Ala Val Gln Gly Arg Arg Arg Pro
 100 105 110

Leu Ala Gly Leu Ala Asp Pro Ala Ala Ala Asp Val Xaa Leu Pro Ala
 115 120 125

Gly Ile Gly
 130

<210> 17

<211> 392

<212> DNA

<213> mycobacterium avium paratuberculosis

<220>

<221> CDS

<222> (94)..(390)

<223>

<400> 17

cggcgtagca tcgtcaagtc gttgcccgcg ctgatgccgg agcggcagta aggagttcgg 60

ctgggtgcaaa aacgcttgcc cacagtcggt ttg gtg ctg acg gcc gtt gtc gcc 114
 Val Leu Thr Ala Val Val Ala
 1 5

ggt atc gcc ggg tgc agc gcg gcg cag acc gtg ccg cgc aag gcc gcc 162
 Gly Ile Ala Gly Cys Ser Ala Ala Gln Thr Val Pro Arg Lys Ala Ala
 10 15 20

cgg ctg acc atc gac ggt gcc acc cac acg acc cgc ccg ccg tcc tgc 210
 Arg Leu Thr Ile Asp Gly Ala Thr His Thr Thr Arg Pro Pro Ser Cys
 25 30 35
 cgg cag gac cag atg tat cgg acc atc aac atc ccc gac cac gac ggt 258
 Arg Gln Asp Gln Met Tyr Arg Thr Ile Asn Ile Pro Asp His Asp Gly
 40 45 50 55
 gga gtc gaa gcg gtg gtg ctg ctc agc ggt tac cgg gtg atg ccg cag 306
 Gly Val Glu Ala Val Val Leu Leu Ser Gly Tyr Arg Val Met Pro Gln
 60 65 70
 tgg gtg aag atc cgg aac gtc gac ggc ttc acc ggc agt cta ctg gcc 354
 Trp Val Lys Ile Arg Asn Val Asp Gly Phe Thr Gly Ser Leu Leu Ala
 75 80 85
 asg gcg gag tgg gcg acg cgc acg tcg atc tca cma at 392
 Xaa Ala Glu Trp Ala Thr Arg Thr Ser Ile Ser Xaa
 90 95

<210> 18

<211> 99

<212> PRT

<213> mycobacterium avium paratuberculosis

<220>

<221> misc_feature

<222> (88)..(88)

<223> The 'Xaa' at location 88 stands for Arg, or Thr.

<220>

<221> misc_feature

<222> (99)..(99)

<223> The 'Xaa' at location 99 stands for Gln, or Pro.

<400> 18

Val Leu Thr Ala Val Val Ala Gly Ile Ala Gly Cys Ser Ala Ala Gln
 1 5 10 15

Thr Val Pro Arg Lys Ala Ala Arg Leu Thr Ile Asp Gly Ala Thr His
 20 25 30

Thr Thr Arg Pro Pro Ser Cys Arg Gln Asp Gln Met Tyr Arg Thr Ile
 35 40 45

Asn Ile Pro Asp His Asp Gly Gly Val Glu Ala Val Val Leu Leu Ser
 50 55 60

Gly Tyr Arg Val Met Pro Gln Trp Val Lys Ile Arg Asn Val Asp Gly
 65 70 75 80

Phe Thr Gly Ser Leu Leu Ala Xaa Ala Glu Trp Ala Thr Arg Thr Ser
 85 90 95

Ile Ser Xaa

<210> 19

<211> 1884

<212> DNA

<213> mycobacterium avium paratuberculosis

<220>

<221> CDS

<222> (13) .. (1884)

<223>

<400> 19

taaccaggag ca atg gct cgt gcg gtc ggt atc gac ctc ggg acc acc aac	51
Met Ala Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn	
1 5 10	
tcc gtc gtc gca gtc ctc gag ggc ggt gac ccc gtc gtc gtc gcc aac	99
Ser Val Val Ala Val Leu Glu Gly Gly Asp Pro Val Val Val Ala Asn	
15 20 25	
tcc gag ggc tcg cgg acc acc ccg tcc atc gtc gcg ttc gcc cgc aac	147
Ser Glu Gly Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn	
30 35 40 45	
ggc gag gtg ctc gtc ggc cag ccc gcc aag aac cag gcg gtg acc aac	195
Gly Glu Val Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn	
50 55 60	
gtc gac cgc acc atc cgt tcg gtc aag cgg cac atg ggc acc gac tgg	243
Val Asp Arg Thr Ile Arg Ser Val Lys Arg His Met Gly Thr Asp Trp	
65 70 75	
tcc atc gag atc gac ggc aag aaa tac acc gct cag gag atc agc gcc	291
Ser Ile Glu Ile Asp Gly Lys Lys Tyr Thr Ala Gln Glu Ile Ser Ala	
80 85 90	
cgc gtg ctg atg aag ctc aag cgc gac gcc gag gcc tat ctg ggt gag	339
Arg Val Leu Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu	
95 100 105	
gac atc acc gac gcg gtc atc acc gta ccg gcg tac ttc aac gac gcc	387
Asp Ile Thr Asp Ala Val Ile Thr Val Pro Ala Tyr Phe Asn Asp Ala	
110 115 120 125	
cag cgt cag gcg acc aag gaa gcc ggc cag atc gcc ggc ctc aac gtg	435
Gln Arg Gln Ala Thr Lys Glu Ala Gly Gln Ile Ala Gly Leu Asn Val	
130 135 140	
ctg cgc atc gtc aac gag ccg acc gcg gcc gcg ctg gcc tac ggc ctg	483

Leu	Arg	Ile	Val	Asn	Glu	Pro	Thr	Ala	Ala	Ala	Leu	Ala	Tyr	Gly	Leu		
			145					150					155				
gac	aag	ggc	gag	aag	gag	cag	acc	atc	ctg	gtc	ttc	gac	ctc	ggc	ggc	531	
Asp	Lys	Gly	Glu	Lys	Glu	Gln	Thr	Ile	Leu	Val	Phe	Asp	Leu	Gly	Gly		
		160					165					170					
ggc	acg	ttc	gac	gtt	tcg	ctg	ctc	gag	atc	ggc	gag	ggg	gtg	gtc	gag	579	
Gly	Thr	Phe	Asp	Val	Ser	Leu	Leu	Glu	Ile	Gly	Glu	Gly	Val	Val	Glu		
	175					180					185						
gtc	cgc	gcc	acc	agc	ggg	gac	aac	caa	ctc	ggg	ggc	gac	gac	tggt	gac	627	
Val	Arg	Ala	Thr	Ser	Gly	Asp	Asn	Gln	Leu	Gly	Gly	Asp	Asp	Trp	Asp		
190					195					200					205		
gac	cgg	atc	gtc	aac	tggt	ctg	gtc	gac	aag	ttc	aag	ggc	acc	agc	ggc	675	
Asp	Arg	Ile	Val	Asn	Trp	Leu	Val	Asp	Lys	Phe	Lys	Gly	Thr	Ser	Gly		
				210					215					220			
atc	gac	ctg	acc	aag	gac	aag	atg	gcc	atg	cag	cgg	ctg	cgt	gag	gcc	723	
Ile	Asp	Leu	Thr	Lys	Asp	Lys	Met	Ala	Met	Gln	Arg	Leu	Arg	Glu	Ala		
			225					230						235			
gcc	gag	aag	gcc	aag	atc	gag	ttg	tcc	agc	tcg	cag	agc	acc	tcg	atc	771	
Ala	Glu	Lys	Ala	Lys	Ile	Glu	Leu	Ser	Ser	Ser	Gln	Ser	Thr	Ser	Ile		
		240					245						250				
aac	ctg	ccc	tac	atc	acc	gtc	gac	gcg	gac	aag	aac	ccg	ctg	ttc	ctc	819	
Asn	Leu	Pro	Tyr	Ile	Thr	Val	Asp	Ala	Asp	Lys	Asn	Pro	Leu	Phe	Leu		
		255				260					265						
gac	gag	cag	ctg	acc	cgc	gcc	gaa	ttc	cag	cgc	atc	acc	cag	gat	ctg	867	
Asp	Glu	Gln	Leu	Thr	Arg	Ala	Glu	Phe	Gln	Arg	Ile	Thr	Gln	Asp	Leu		
		270			275					280					285		
ctg	gac	cgc	acc	cgt	cag	ccg	ttc	aag	tcg	gtg	atc	gcc	gac	gcc	ggc	915	
Leu	Asp	Arg	Thr	Arg	Gln	Pro	Phe	Lys	Ser	Val	Ile	Ala	Asp	Ala	Gly		
				290					295					300			
atc	tcg	gtg	tcc	gac	atc	gac	cac	gtg	gtg	ctg	gtg	ggg	ggg	tcc	acc	963	
Ile	Ser	Val	Ser	Asp	Ile	Asp	His	Val	Val	Leu	Val	Gly	Gly	Ser	Thr		
			305					310					315				
cgg	atg	ccc	gcg	gtg	acc	gac	ctg	gtc	aag	gaa	ctc	acc	ggc	ggc	aag	1011	
Arg	Met	Pro	Ala	Val	Thr	Asp	Leu	Val	Lys	Glu	Leu	Thr	Gly	Gly	Lys		
			320				325						330				
gag	ccc	aac	aag	ggc	gtc	aac	ccc	gac	gag	gtt	gtc	gcg	gtg	ggg	gcc	1059	
Glu	Pro	Asn	Lys	Gly	Val	Asn	Pro	Asp	Glu	Val	Val	Ala	Val	Gly	Ala		
		335				340					345						
gcc	ctg	cag	gcc	ggg	gtg	ctt	aag	ggc	gag	gtg	aaa	gac	gtt	ctg	ctg	1107	
Ala	Leu	Gln	Ala	Gly	Val	Leu	Lys	Gly	Glu	Val	Lys	Asp	Val	Leu	Leu		
		350			355					360					365		
ctt	gac	gtt	acg	ccg	ctg	agc	ctg	ggg	atc	gag	acc	aag	ggg	ggc	gtg	1155	
Leu	Asp	Val	Thr	Pro	Leu	Ser	Leu	Gly	Ile	Glu	Thr	Lys	Gly	Gly	Val		
				370					375					380			
atg	acc	aag	ctg	atc	gaa	cgc	aac	acc	acc	atc	ccg	acc	aag	cgg	tcc	1203	
Met	Thr	Lys	Leu	Ile	Glu	Arg	Asn	Thr	Thr	Ile	Pro	Thr	Lys	Arg	Ser		
			385					390						395			
gag	acg	ttc	acc	acg	gcc	gac	gac	aac	cag	ccg	tcg	gtg	cag	atc	cag	1251	
Glu	Thr	Phe	Thr	Thr	Ala	Asp	Asp	Asn	Gln	Pro	Ser	Val	Gln	Ile	Gln		
		400					405					410					
gtg	tat	cag	ggg	gag	cgc	gaa	atc	gcc	gcg	cac	aac	aag	ctg	ctc	ggc	1299	

Val Tyr Gln Gly Glu Arg Glu Ile Ala Ala His Asn Lys Leu Leu Gly	
415 420 425	
tcc ttc gag ctg acc gga att ccg ccg gcg ccc cgc gcc gtg ccg cag	1347
Ser Phe Glu Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly Val Pro Gln	
430 435 440 445	
atc gag gtc acc ttc gac atc gac gcc aac gcc atc gtg cac gtc acc	1395
Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Val His Val Thr	
450 455 460	
gcc aag gac aag gcc acc ggt aag gag aac acg atc aag atc cag gag	1443
Ala Lys Asp Lys Gly Thr Gly Lys Glu Asn Thr Ile Lys Ile Gln Glu	
465 470 475	
ggc tcc gcc ctg tcc aag gag gag atc gac cgg atg atc aag gac gcc	1491
Gly Ser Gly Leu Ser Lys Glu Glu Ile Asp Arg Met Ile Lys Asp Ala	
480 485 490	
gag gcg cac gcc gag gag gac cgc aag agg cgc gag gaa gcc gac gtc	1539
Glu Ala His Ala Glu Glu Asp Arg Lys Arg Arg Glu Glu Ala Asp Val	
495 500 505	
cgc aac caa gcg gaa tcg ctt gtc tac cag acg gag aag ttc gtc aag	1587
Arg Asn Gln Ala Glu Ser Leu Val Tyr Gln Thr Glu Lys Phe Val Lys	
510 515 520 525	
gac cag cgc gag gcc gag gcc ggc tgc aag gtt ccc gag gag acg ctg	1635
Asp Gln Arg Glu Ala Glu Gly Gly Ser Lys Val Pro Glu Glu Thr Leu	
530 535 540	
tcc aag gtc gac gcc gcg atc gcc gac gcc aag acg gcc ctg gcc gcc	1683
Ser Lys Val Asp Ala Ala Ile Ala Asp Ala Lys Thr Ala Leu Gly Gly	
545 550 555	
acc gac atc acc gcg atc aag tcg gcg atg gag aag ctc gcc cag gag	1731
Thr Asp Ile Thr Ala Ile Lys Ser Ala Met Glu Lys Leu Gly Gln Glu	
560 565 570	
tcg caa gcg ctg gga cag gca atc tac gag gcc acc cag gcc gag tcc	1779
Ser Gln Ala Leu Gly Gln Ala Ile Tyr Glu Ala Thr Gln Ala Glu Ser	
575 580 585	
gcc cag gct gcc ggg ccg gac ggt gcc gcg gcc gcc gcc ggc ggc tcc gga	1827
Ala Gln Ala Gly Gly Pro Asp Gly Ala Ala Ala Gly Gly Gly Ser Gly	
590 595 600 605	
tcc gcc gac gat gtt gtg gac gcg gag gtg gtc gac gat gac cgg gag	1875
Ser Ala Asp Asp Val Val Asp Ala Glu Val Val Asp Asp Asp Arg Glu	
610 615 620	
tcc aag tga	1884
Ser Lys	

<210> 20

<211> 623

<212> PRT

<213> mycobacterium avium paratuberculosis

<400> 20

Met Ala Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val
 1 5 10 15
 Ala Val Leu Glu Gly Gly Asp Pro Val Val Val Ala Asn Ser Glu Gly
 20 25 30
 Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn Gly Glu Val
 35 40 45
 Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
 50 55 60
 Thr Ile Arg Ser Val Lys Arg His Met Gly Thr Asp Trp Ser Ile Glu
 65 70 75 80
 Ile Asp Gly Lys Lys Tyr Thr Ala Gln Glu Ile Ser Ala Arg Val Leu
 85 90 95
 Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Ile Thr
 100 105 110
 Asp Ala Val Ile Thr Val Pro Ala Tyr Phe Asn Asp Ala Gln Arg Gln
 115 120 125
 Ala Thr Lys Glu Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
 130 135 140
 Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Asp Lys Gly
 145 150 155 160
 Glu Lys Glu Gln Thr Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
 165 170 175
 Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala
 180 185 190
 Thr Ser Gly Asp Asn Gln Leu Gly Gly Asp Asp Trp Asp Asp Arg Ile
 195 200 205
 Val Asn Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Ile Asp Leu
 210 215 220
 Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys
 225 230 235 240
 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro
 245 250 255
 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
 260 265 270

Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg
275 280 285

Thr Arg Gln Pro Phe Lys Ser Val Ile Ala Asp Ala Gly Ile Ser Val
290 295 300

Ser Asp Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
305 310 315 320

Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn
325 330 335

Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
340 345 350

Ala Gly Val Leu Lys Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val
355 360 365

Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys
370 375 380

Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
385 390 395 400

Thr Thr Ala Asp Asp Asn Gln Pro Ser Val Gln Ile Gln Val Tyr Gln
405 410 415

Gly Glu Arg Glu Ile Ala Ala His Asn Lys Leu Leu Gly Ser Phe Glu
420 425 430

Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val
435 440 445

Thr Phe Asp Ile Asp Ala Asn Gly Ile Val His Val Thr Ala Lys Asp
450 455 460

Lys Gly Thr Gly Lys Glu Asn Thr Ile Lys Ile Gln Glu Gly Ser Gly
465 470 475 480

Leu Ser Lys Glu Glu Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His
485 490 495

Ala Glu Glu Asp Arg Lys Arg Arg Glu Glu Ala Asp Val Arg Asn Gln
500 505 510

Ala Glu Ser Leu Val Tyr Gln Thr Glu Lys Phe Val Lys Asp Gln Arg
515 520 525

Glu Ala Glu Gly Gly Ser Lys Val Pro Glu Glu Thr Leu Ser Lys Val
530 535 540

25/29

Asp Ala Ala Ile Ala Asp Ala Lys Thr Ala Leu Gly Gly Thr Asp Ile
545 550 555 560

Thr Ala Ile Lys Ser Ala Met Glu Lys Leu Gly Gln Glu Ser Gln Ala
565 570 575

Leu Gly Gln Ala Ile Tyr Glu Ala Thr Gln Ala Glu Ser Ala Gln Ala
580 585 590

Gly Gly Pro Asp Gly Ala Ala Ala Gly Gly Gly Ser Gly Ser Ala Asp
595 600 605

Asp Val Val Asp Ala Glu Val Val Asp Asp Asp Arg Glu Ser Lys
610 615 620

<210> 21

<211> 1701

<212> DNA

<213> mycobacterium avium paratuberculosis

<220>

<221> CDS

<222> (76)..(1701)

<223>

<400> 21

gcagcctggt cgccgctgcg gggcactgca cccggccagg acgtgtcatc cccaatccgg 60

aggaatcact tcgca atg gcc aag aca att gcg tac gac gaa gag gcc cgt 111
Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg
1 5 10

cgc ggc ctc gag cgg ggg ctc aac gcc ctc gcc gac gcg gta aag gtc 159
Arg Gly Leu Glu Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val
15 20 25

acg ttg ggc ccc aag ggt cgc aac gtc gtc ctg gag aag aag tgg ggt 207
Thr Leu Gly Pro Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly
30 35 40

gcc ccc acg atc acc aac gat ggt gtg tcc atc gcc aag gag atc gag 255
Ala Pro Thr Ile Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu
45 50 55 60

ctg gag gac ccg tac gag aag atc ggc gcc gag ctg gtc aag gaa gtc 303
Leu Glu Asp Pro Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val
65 70 75

gcc aag aag acc gac gac gtc gcc ggt gac ggc acg acg acg gcc acg 351
Ala Lys Lys Thr Asp Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr
80 85 90

gtg ctc gcc cag gcg ttg gtc cgc gag ggc ctg cgc aac gtc gcg gcc 399

Val	Leu	Ala	Gln	Ala	Leu	Val	Arg	Glu	Gly	Leu	Arg	Asn	Val	Ala	Ala		
	95						100					105					
ggc	gcc	aac	ccg	ctg	ggt	ctc	aag	cgc	ggc	atc	gag	aag	gcc	gtc	gag		447
Gly	Ala	Asn	Pro	Leu	Gly	Leu	Lys	Arg	Gly	Ile	Glu	Lys	Ala	Val	Glu		
	110					115					120						
aag	gtc	acc	gag	acc	ctg	ctc	aag	tcg	gcc	aag	gag	gtc	gag	acc	aag		495
Lys	Val	Thr	Glu	Thr		Leu	Leu	Lys	Ser	Ala	Lys	Glu	Val	Glu	Thr	Lys	
	125					130					135					140	
gac	cag	atc	gct	gcc	acc	gcg	gcc	atc	tcc	gcg	ggc	gac	cag	tcg	atc		543
Asp	Gln	Ile	Ala	Ala	Thr	Ala	Ala	Ile	Ser	Ala	Gly	Asp	Gln	Ser	Ile		
					145					150					155		
ggc	gac	ctg	atc	gcc	gag	gcg	atg	gac	aag	gtc	ggc	aac	gag	ggc	gtc		591
Gly	Asp	Leu	Ile	Ala	Glu	Ala	Met	Asp	Lys	Val	Gly	Asn	Glu	Gly	Val		
			160					165					170				
atc	acc	gtc	gag	gag	tcc	aac	acc	ttc	ggc	ctg	cag	ctc	gag	ctc	acc		639
Ile	Thr	Val	Glu	Glu	Ser	Asn	Thr	Phe	Gly	Leu	Gln	Leu	Glu	Leu	Thr		
			175				180					185					
gag	ggt	atg	cgg	ttc	gac	aag	ggt	tac	atc	tcg	ggc	tac	ttc	gtc	acg		687
Glu	Gly	Met	Arg	Phe	Asp	Lys	Gly	Tyr	Ile	Ser	Gly	Tyr	Phe	Val	Thr		
	190					195					200						
gac	gcc	gag	cgt	cag	gaa	gcg	gtc	ctc	gag	gac	ccg	ttc	atc	ctg	ctg		735
Asp	Ala	Glu	Arg	Gln	Glu	Ala	Val	Leu	Glu	Asp	Pro	Phe	Ile	Leu	Leu		
	205				210					215					220		
gtc	agc	tcc	aag	gtc	tcg	acc	gtc	aag	gac	ctg	ctg	ccg	ctg	ctg	gag		783
Val	Ser	Ser	Lys	Val	Ser	Thr	Val	Lys	Asp	Leu	Leu	Pro	Leu	Leu	Glu		
					225				230					235			
aag	gtc	atc	cag	gcc	ggc	aag	ccg	ctg	ctg	atc	atc	gcc	gag	gac	gtc		831
Lys	Val	Ile	Gln	Ala	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val		
			240					245					250				
gag	ggc	gag	gcc	ctg	tcc	acc	ctg	gtc	gtc	aac	aag	atc	cgc	ggc	acc		879
Glu	Gly	Glu	Ala	Leu	Ser	Thr	Leu	Val	Val	Asn	Lys	Ile	Arg	Gly	Thr		
			255				260					265					
ttc	aag	tcg	gtg	gcc	gtc	aag	gcg	ccc	ggc	ttc	ggc	gac	cgc	cgc	aag		927
Phe	Lys	Ser	Val	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys		
	270					275					280						
gcg	atg	ctt	cag	gac	atg	gcc	atc	ctc	acc	ggc	ggc	cag	gtc	atc	agc		975
Ala	Met	Leu	Gln	Asp	Met	Ala	Ile	Leu	Thr	Gly	Gly	Gln	Val	Ile	Ser		
	285				290					295					300		
gaa	gag	gtc	ggc	ctg	tcg	ctg	gag	agc	gcc	gac	atc	tcg	ctg	ctc	ggt		1023
Glu	Glu	Val	Gly	Leu	Ser	Leu	Glu	Ser	Ala	Asp	Ile	Ser	Leu	Leu	Gly		
				305					310					315			
aag	gcc	cgc	aag	gtc	gtc	gtc	acc	aag	gac	gag	acc	acc	atc	gtc	gag		1071
Lys	Ala	Arg	Lys	Val	Val	Val	Thr	Lys	Asp	Glu	Thr	Thr	Ile	Val	Glu		
				320				325					330				
ggc	gcc	ggt	gac	tcc	gac	gcc	atc	gcc	ggc	cgc	gtg	gcc	cag	atc	cgc		1119
Gly	Ala	Gly	Asp	Ser	Asp	Ala	Ile	Ala	Gly	Arg	Val	Ala	Gln	Ile	Arg		
			335				340					345					
acc	gag	atc	gag	aac	agc	gac	tcc	gac	tac	gac	cgc	gag	aag	ctg	cag		1167
Thr	Glu	Ile	Glu	Asn	Ser	Asp	Ser	Asp	Tyr	Asp	Arg	Glu	Lys	Leu	Gln		
			350			355					360						
gag	cgc	ctg	gcc	aag	ctg	gcc	ggc	ggc	gtg	gcg	gtg	atc	aag	gcc	ggc		1215

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Glu Arg Leu Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Ala Gly	
365 370 375 380	
gcc gcg acc gag gtc gag ctc aag gag cgc aag cac cgc atc gag gac	1263
Ala Ala Thr Glu Val Glu Leu Lys Glu Arg Lys His Arg Ile Glu Asp	
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Ala Val Arg Asn Ala Lys Ala Ala Val Glu Glu Gly Ile Val Ala Gly	
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ggt ggc gtg gcc ctg ctg cac gcg atc ccg gct ctg gac gag ctg aag	1359
Gly Gly Val Ala Leu Leu His Ala Ile Pro Ala Leu Asp Glu Leu Lys	
415 420 425	
ctc gag ggc gaa gag gcg acc ggc gcc aac atc gtc cgg gtg gcc ctc	1407
Leu Glu Gly Glu Glu Ala Thr Gly Ala Asn Ile Val Arg Val Ala Leu	
430 435 440	
gag gct ccg ctg aag cag atc gcc ttc aac ggt ggc ctg gag ccc gcc	1455
Glu Ala Pro Leu Lys Gln Ile Ala Phe Asn Gly Gly Leu Glu Pro Gly	
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Val Val Ala Glu Lys Val Arg Asn Ser Pro Ala Gly Thr Gly Leu Asn	
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gcc gcc acc ggt gag tac gag gac ctg ctc aag gcc ggc att gcc gac	1551
Ala Ala Thr Gly Glu Tyr Glu Asp Leu Leu Lys Ala Gly Ile Ala Asp	
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ccg gtg aag gtc acc cgc tcg gcg ctg cag aac gcg gcg tcc atc gcg	1599
Pro Val Lys Val Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala	
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Gly Leu Phe Leu Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys	
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gcg gcc gct ccc gcg ggc gac ccg acc ggc ggc atg ggc ggc atg gac	1695
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ttc tga	1701
Phe	

<210> 22

<211> 541

<212> PRT

<213> mycobacterium avium paratuberculosis

<400> 22

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20 25 30

Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala Pro Thr Ile
 35 40 45
 Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu Leu Glu Asp Pro
 50 55 60
 Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val Ala Lys Lys Thr
 65 70 75 80
 Asp Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln
 85 90 95
 Ala Leu Val Arg Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro
 100 105 110
 Leu Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Glu Lys Val Thr Glu
 115 120 125
 Thr Leu Leu Lys Ser Ala Lys Glu Val Glu Thr Lys Asp Gln Ile Ala
 130 135 140
 Ala Thr Ala Ala Ile Ser Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile
 145 150 155 160
 Ala Glu Ala Met Asp Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu
 165 170 175
 Glu Ser Asn Thr Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg
 180 185 190
 Phe Asp Lys Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Ala Glu Arg
 195 200 205
 Gln Glu Ala Val Leu Glu Asp Pro Phe Ile Leu Leu Val Ser Ser Lys
 210 215 220
 Val Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gln
 225 230 235 240
 Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Ala
 245 250 255
 Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr Phe Lys Ser Val
 260 265 270
 Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Gln
 275 280 285
 Asp Met Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Val Gly
 290 295 300

Leu Ser Leu Glu Ser Ala Asp Ile Ser Leu Leu Gly Lys Ala Arg Lys
 305 310 315 320
 Val Val Val Thr Lys Asp Glu Thr Thr Ile Val Glu Gly Ala Gly Asp
 325 330 335
 Ser Asp Ala Ile Ala Gly Arg Val Ala Gln Ile Arg Thr Glu Ile Glu
 340 345 350
 Asn Ser Asp Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala
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 Lys Leu Ala Gly Gly Val Ala Val Ile Lys Ala Gly Ala Ala Thr Glu
 370 375 380
 Val Glu Leu Lys Glu Arg Lys His Arg Ile Glu Asp Ala Val Arg Asn
 385 390 395 400
 Ala Lys Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Val Ala
 405 410 415
 Leu Leu His Ala Ile Pro Ala Leu Asp Glu Leu Lys Leu Glu Gly Glu
 420 425 430
 Glu Ala Thr Gly Ala Asn Ile Val Arg Val Ala Leu Glu Ala Pro Leu
 435 440 445
 Lys Gln Ile Ala Phe Asn Gly Gly Leu Glu Pro Gly Val Val Ala Glu
 450 455 460
 Lys Val Arg Asn Ser Pro Ala Gly Thr Gly Leu Asn Ala Ala Thr Gly
 465 470 475 480
 Glu Tyr Glu Asp Leu Leu Lys Ala Gly Ile Ala Asp Pro Val Lys Val
 485 490 495
 Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu Phe Leu
 500 505 510
 Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Ala Ala Ala Pro
 515 520 525
 Ala Gly Asp Pro Thr Gly Gly Met Gly Gly Met Asp Phe
 530 535 540